> **This Raw Listing contains the General Information Section and up to first 5 pages.**

ENTERED

```
 1    <110> APPLICANT: Georgopoulos, Katia
 2          Mogan, Bruce A.
 3          Kelly, Clair
 4    <120> TITLE OF INVENTION: THE HELIOS GENE
 5    <130> FILE REFERENCE: 10287/043001
 6    <140> CURRENT APPLICATION NUMBER: US/09/259,389
 7    <141> CURRENT FILING DATE: 1999-02-26
 8    <150> EARLIER APPLICATION NUMBER: US 60/076,325
 9    <151> EARLIER FILING DATE: 1998-02-27
10    <160> NUMBER OF SEQ ID NOS: 17
11    <170> SOFTWARE: FastSEQ for Windows Version 3.0
12    <210> SEQ ID NO 1
13    <211> LENGTH: 1598
14    <212> TYPE: DNA
15    <213> ORGANISM: Mus musculus
16    <220> FEATURE:
17    <221> NAME/KEY: CDS
18    <222> LOCATION: (1)...(1578)
19    <400> SEQUENCE: 1
20          atg gaa aca gac gct att gat ggc tat ata aca tgt gac aat gag ctt        48
21          Met Glu Thr Asp Ala Ile Asp Gly Tyr Ile Thr Cys Asp Asn Glu Leu
22           1               5                  10                  15
23          tca ccc gaa ggg gaa cac gcc aat atg gcc att gac ctc acc tca agc        96
24          Ser Pro Glu Gly Glu His Ala Asn Met Ala Ile Asp Leu Thr Ser Ser
25                          20                  25                  30
26          acg ccc aat gga cag cac gcc tcg cca agt cac atg aca agc aca aat       144
27          Thr Pro Asn Gly Gln His Ala Ser Pro Ser His Met Thr Ser Thr Asn
28                          35                  40                  45
29          tct gta aag ctg gaa atg cag agt gat gaa gag tgt gac agg cag ccc       192
30          Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg Gln Pro
31                          50                  55                  60
32          ctg agc cgt gag gat gag atc agg ggc cac gat gag ggg agc agc cta       240
33          Leu Ser Arg Glu Asp Glu Ile Arg Gly His Asp Glu Gly Ser Ser Leu
34           65                  70                  75                  80
35          gaa gaa ccc cta att gag agc agc gag gtg gcc gac aac agg aaa gtc       288
36          Glu Glu Pro Leu Ile Glu Ser Ser Glu Val Ala Asp Asn Arg Lys Val
37                              85                  90                  95
38          cag gac ctt caa ggc gag gga gga atc cgg ctt ccg aat ggt aaa ctg       336
39          Gln Asp Leu Gln Gly Glu Gly Gly Ile Arg Leu Pro Asn Gly Lys Leu
40                          100                 105                 110
41          aaa tgt gac gtc tgt ggc atg gtt tgc att ggg ccc aat gtg ctt atg       384
42          Lys Cys Asp Val Cys Gly Met Val Cys Ile Gly Pro Asn Val Leu Met
43                          115                 120                 125
44          gta cat aaa agg agt cac act ggt gag cgg ccc ttc cac tgt aac cag       432
```

```
45        Val His Lys Arg Ser His Thr Gly Glu Arg Pro Phe His Cys Asn Gln
46            130                 135             140
47        tgc gga gct tct ttt acc cag aag ggc aac ctt ctg aga cac ata aag        480
48        Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys
49        145                 150                 155                 160
50        tta cac tct gga gag aag ccc ttc aaa tgt cct ttc tgt agc tat gct        528
51        Leu His Ser Gly Glu Lys Pro Phe Lys Cys Pro Phe Cys Ser Tyr Ala
52                        165                 170                 175
53        tgt aga aga agg gac gct ctc aca gga cac ctc agg acc cat tct gtg        576
54        Cys Arg Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val
55                        180                 185                 190
56        ggt aaa cct cac aag tgt aac tac tgt ggc cga agc tac aag cag cgc        624
57        Gly Lys Pro His Lys Cys Asn Tyr Cys Gly Arg Ser Tyr Lys Gln Arg
58                        195                 200                 205
59        acg tca ctg gag gaa cac aag gaa cgc tgt cac aac tat ctc cag aat        672
60        Thr Ser Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu Gln Asn
61            210                 215                 220
62        gtc agc atg gag gct gcc ggg cag gtc atg agt cac cat gta ccg cct        720
63        Val Ser Met Glu Ala Ala Gly Gln Val Met Ser His His Val Pro Pro
64        225                 230                 235                 240
65        atg gaa gat tgt aag gaa caa gag cct atc atg gac aac aat att tct        768
66        Met Glu Asp Cys Lys Glu Gln Glu Pro Ile Met Asp Asn Asn Ile Ser
67                        245                 250                 255
68        ctg gtg cct ttt gag aga cct gct gtc ata gag aag ctc acg gca aat        816
69        Leu Val Pro Phe Glu Arg Pro Ala Val Ile Glu Lys Leu Thr Ala Asn
70                        260                 265                 270
71        atg gga aag cgc aaa agc tcc act cct cag aag ttt gtg ggg gaa aag        864
72        Met Gly Lys Arg Lys Ser Ser Thr Pro Gln Lys Phe Val Gly Glu Lys
73                        275                 280                 285
74        ctt atg cga ttc agc tac cca gat att cat ttt gat atg aac tta aca        912
75        Leu Met Arg Phe Ser Tyr Pro Asp Ile His Phe Asp Met Asn Leu Thr
76            290                 295                 300
77        tat gag aag gag gct gag ctg atg cag tct cat atg atg gac caa gcc        960
78        Tyr Glu Lys Glu Ala Glu Leu Met Gln Ser His Met Met Asp Gln Ala
79        305                 310                 315                 320
80        atc aac aat gca atc acc tac ctt gga gct gag gcc ctt cac cct ctg       1008
81        Ile Asn Asn Ala Ile Thr Tyr Leu Gly Ala Glu Ala Leu His Pro Leu
82                        325                 330                 335
83        atg cag cat gca cca agc aca atc gct gag gtg gcc cca gtt ata agc       1056
84        Met Gln His Ala Pro Ser Thr Ile Ala Glu Val Ala Pro Val Ile Ser
85                        340                 345                 350
86        tca gct tat tct cag gtc tat cat cca aac agg ata gaa aga ccc att       1104
87        Ser Ala Tyr Ser Gln Val Tyr His Pro Asn Arg Ile Glu Arg Pro Ile
88                        355                 360                 365
89        agc agg gaa aca tct gat agt cac gaa aac aac atg gat ggc ccc atc       1152
90        Ser Arg Glu Thr Ser Asp Ser His Glu Asn Asn Met Asp Gly Pro Ile
91            370                 375                 380
92        tct ctc atc aga cca aag agt cga ccc cag gaa aga gag gcc tcg ccc       1200
93        Ser Leu Ile Arg Pro Lys Ser Arg Pro Gln Glu Arg Glu Ala Ser Pro
94        385                 390                 395                 400
```

```
 95        agc aat agc tgc ctc gat tct act gac tca gaa agt agc cat gat gac       1248
 96        Ser Asn Ser Cys Leu Asp Ser Thr Asp Ser Glu Ser Ser His Asp Asp
 97                        405                 410                 415
 98        cgc cag tcc tac caa gga aac cct gcc tta aat ccc aag agg aaa caa       1296
 99        Arg Gln Ser Tyr Gln Gly Asn Pro Ala Leu Asn Pro Lys Arg Lys Gln
100                        420                 425                 430
101        agc cca gct tac atg aag gag gat gtc aag gct ttg gat gct acc aag       1344
102        Ser Pro Ala Tyr Met Lys Glu Asp Val Lys Ala Leu Asp Ala Thr Lys
103                        435                 440                 445
104        gcc ccc aag ggc tct ctg aag gac atc tat aag gtt ttc aat gga gaa       1392
105        Ala Pro Lys Gly Ser Leu Lys Asp Ile Tyr Lys Val Phe Asn Gly Glu
106                        450                 455                 460
107        gga gaa cag ata agg gcc ttc aag tgt gag cac tgc cga gtc ctt ttt       1440
108        Gly Glu Gln Ile Arg Ala Phe Lys Cys Glu His Cys Arg Val Leu Phe
109        465                 470                 475                 480
110        cta gac cat gtc atg tac acc att cac atg ggt tgc cat ggc tac cgg       1488
111        Leu Asp His Val Met Tyr Thr Ile His Met Gly Cys His Gly Tyr Arg
112                        485                 490                 495
113        gac cca ctg gaa tgc aac atc tgt ggc tac aga agc cag gac cgc tac       1536
114        Asp Pro Leu Glu Cys Asn Ile Cys Gly Tyr Arg Ser Gln Asp Arg Tyr
115                        500                 505                 510
116        gaa ttt tca tca cac att gtt ggg ggg cag cac aca ttc cac             1578
117        Glu Phe Ser Ser His Ile Val Gly Gly Gln His Thr Phe His
118                        515                 520                 525
119        taggcgtttg cattccaagg                                               1598
120   <210> SEQ ID NO 2
121   <211> LENGTH: 526
122   <212> TYPE: PRT
123   <213> ORGANISM: Mus musculus
124   <400> SEQUENCE: 2
125        Met Glu Thr Asp Ala Ile Asp Gly Tyr Ile Thr Cys Asp Asn Glu Leu
126         1               5                  10                  15
127        Ser Pro Glu Gly Glu His Ala Asn Met Ala Ile Asp Leu Thr Ser Ser
128                         20                 25                  30
129        Thr Pro Asn Gly Gln His Ala Ser Pro Ser His Met Thr Ser Thr Asn
130                         35                 40                  45
131        Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg Gln Pro
132                 50                 55                  60
133        Leu Ser Arg Glu Asp Glu Ile Arg Gly His Asp Glu Gly Ser Ser Leu
134         65                 70                  75                  80
135        Glu Glu Pro Leu Ile Glu Ser Ser Glu Val Ala Asp Asn Arg Lys Val
136                         85                 90                  95
137        Gln Asp Leu Gln Gly Glu Gly Gly Ile Arg Leu Pro Asn Gly Lys Leu
138                        100                105                 110
139        Lys Cys Asp Val Cys Gly Met Val Cys Ile Gly Pro Asn Val Leu Met
140                        115                120                 125
141        Val His Lys Arg Ser His Thr Gly Glu Arg Pro Phe His Cys Asn Gln
142                        130                135                 140
143        Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys
144        145                150                155                 160
```

```
145          Leu His Ser Gly Glu Lys Pro Phe Lys Cys Pro Phe Cys Ser Tyr Ala
146                          165                 170                 175
147          Cys Arg Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val
148                          180                 185                 190
149          Gly Lys Pro His Lys Cys Asn Tyr Cys Gly Arg Ser Tyr Lys Gln Arg
150                          195                 200                 205
151          Thr Ser Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu Gln Asn
152                  210                 215                 220
153          Val Ser Met Glu Ala Ala Gly Gln Val Met Ser His His Val Pro Pro
154          225                 230                 235                 240
155          Met Glu Asp Cys Lys Glu Gln Glu Pro Ile Met Asp Asn Asn Ile Ser
156                          245                 250                 255
157          Leu Val Pro Phe Glu Arg Pro Ala Val Ile Glu Lys Leu Thr Ala Asn
158                          260                 265                 270
159          Met Gly Lys Arg Lys Ser Ser Thr Pro Gln Lys Phe Val Gly Glu Lys
160                          275                 280                 285
161          Leu Met Arg Phe Ser Tyr Pro Asp Ile His Phe Asp Met Asn Leu Thr
162                  290                 295                 300
163          Tyr Glu Lys Glu Ala Glu Leu Met Gln Ser His Met Met Asp Gln Ala
164          305                 310                 315                 320
165          Ile Asn Asn Ala Ile Thr Tyr Leu Gly Ala Glu Ala Leu His Pro Leu
166                          325                 330                 335
167          Met Gln His Ala Pro Ser Thr Ile Ala Glu Val Ala Pro Val Ile Ser
168                          340                 345                 350
169          Ser Ala Tyr Ser Gln Val Tyr His Pro Asn Arg Ile Glu Arg Pro Ile
170                          355                 360                 365
171          Ser Arg Glu Thr Ser Asp Ser His Glu Asn Asn Met Asp Gly Pro Ile
172                  370                 375                 380
173          Ser Leu Ile Arg Pro Lys Ser Arg Pro Gln Glu Arg Glu Ala Ser Pro
174          385                 390                 395                 400
175          Ser Asn Ser Cys Leu Asp Ser Thr Asp Ser Glu Ser Ser His Asp Asp
176                          405                 410                 415
177          Arg Gln Ser Tyr Gln Gly Asn Pro Ala Leu Asn Pro Lys Arg Lys Gln
178                  420                 425                 430
179          Ser Pro Ala Tyr Met Lys Glu Asp Val Lys Ala Leu Asp Ala Thr Lys
180                          435                 440                 445
181          Ala Pro Lys Gly Ser Leu Lys Asp Ile Tyr Lys Val Phe Asn Gly Glu
182                  450                 455                 460
183          Gly Glu Gln Ile Arg Ala Phe Lys Cys Glu His Cys Arg Val Leu Phe
184          465                 470                 475                 480
185          Leu Asp His Val Met Tyr Thr Ile His Met Gly Cys His Gly Tyr Arg
186                          485                 490                 495
187          Asp Pro Leu Glu Cys Asn Ile Cys Gly Tyr Arg Ser Gln Asp Arg Tyr
188                  500                 505                 510
189          Glu Phe Ser Ser His Ile Val Gly Gly Gln His Thr Phe His
190                  515                 520                 525
191  <210> SEQ ID NO 3
192  <211> LENGTH: 1520
193  <212> TYPE: DNA
194  <213> ORGANISM: Mus musculus
```

```
195   <220> FEATURE:
196   <221> NAME/KEY: CDS
197   <222> LOCATION: (1)...(1500)
198   <400> SEQUENCE: 3
199       atg gaa aca gac gct att gat ggc tat ata aca tgt gac aat gag ctt        48
200       Met Glu Thr Asp Ala Ile Asp Gly Tyr Ile Thr Cys Asp Asn Glu Leu
201        1               5                  10                  15
202       tca ccc gaa ggg gaa cac gcc aat atg gcc att gac ctc acc tca agc        96
203       Ser Pro Glu Gly Glu His Ala Asn Met Ala Ile Asp Leu Thr Ser Ser
204                      20                  25                  30
205       acg ccc aat gga cag cac gcc tcg cca agt cac atg aca agc aca aat       144
206       Thr Pro Asn Gly Gln His Ala Ser Pro Ser His Met Thr Ser Thr Asn
207                  35                  40                  45
208       tct gta aag ctg gaa atg cag agt gat gaa gag tgt gac agg cag ccc       192
209       Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg Gln Pro
210              50                  55                  60
211       ctg agc cgt gag gat gag atc agg ggc cac gat gag ggg agc agc cta       240
212       Leu Ser Arg Glu Asp Glu Ile Arg Gly His Asp Glu Gly Ser Ser Leu
213          65                  70                  75                  80
214       gaa gaa ccc cta att gag agc agc gag gtg gcc gac aac agg aaa gtc       288
215       Glu Glu Pro Leu Ile Glu Ser Ser Glu Val Ala Asp Asn Arg Lys Val
216                      85                  90                  95
217       cag gac ctt caa ggc gag gga gga atc cgg ctt ccg aat ggt gag cgg       336
218       Gln Asp Leu Gln Gly Glu Gly Gly Ile Arg Leu Pro Asn Gly Glu Arg
219                  100                 105                 110
220       ccc ttc cac tgt aac cag tgc gga gct tct ttt acc cag aag ggc aac       384
221       Pro Phe His Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn
222              115                 120                 125
223       ctt ctg aga cac ata aag tta cac tct gga gag aag ccc ttc aaa tgt       432
224       Leu Leu Arg His Ile Lys Leu His Ser Gly Glu Lys Pro Phe Lys Cys
225          130                 135                 140
226       cct ttc tgt agc tat gct tgt aga aga agg gac gct ctc aca gga cac       480
227       Pro Phe Cys Ser Tyr Ala Cys Arg Arg Arg Asp Ala Leu Thr Gly His
228       145                 150                 155                 160
229       ctc agg acc cat tct gtg ggt aaa cct cac aag tgt aac tac tgt ggc       528
230       Leu Arg Thr His Ser Val Gly Lys Pro His Lys Cys Asn Tyr Cys Gly
231                      165                 170                 175
232       cga agc tac aag cag cgc acg tca ctg gag gaa cac aag gaa cgc tgt       576
233       Arg Ser Tyr Lys Gln Arg Thr Ser Leu Glu Glu His Lys Glu Arg Cys
234                  180                 185                 190
235       cac aac tat ctc cag aat gtc agc atg gag gct gcc ggg cag gtc atg       624
236       His Asn Tyr Leu Gln Asn Val Ser Met Glu Ala Ala Gly Gln Val Met
237              195                 200                 205
238       agt cac cat gta ccg cct atg gaa gat tgt aag gaa caa gag cct atc       672
239       Ser His His Val Pro Pro Met Glu Asp Cys Lys Glu Gln Glu Pro Ile
240          210                 215                 220
241       atg gac aac aat att tct ctg gtg cct ttt gag aga cct gct gtc ata       720
242       Met Asp Asn Asn Ile Ser Leu Val Pro Phe Glu Arg Pro Ala Val Ile
243       225                 230                 235                 240
244       gag aag ctc acg gca aat atg gga aag cgc aaa agc tcc act cct cag       768
```

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/259,389**

DATE: 03/15/1999
TIME: 14:17:32

Input Set: **I259389.RAW**

Line	?	Error/Warning	Original Text

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/259,389**

DATE: 03/15/1999
TIME: 14:17:32